

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCC  
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAAGCTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTGCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCCGGAATTACCCTTTAAATTATTCAGAAGGATGTCC  
CGTGGAATAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGTTGTTCTTA  
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTTGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTTT

## FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFVCVKTLLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDE  
GACVDVDECAAEPPPCSAQAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

### FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC  
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCCTGTCCTTGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAACACAGGATGGGGTGGCAGCATTGGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTTAAACATGTCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCTGTATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCCAACAACCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT  
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA  
TGTGTTGAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTAAGTTTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGT  
GTCTGGGGGCAGGGGAACATCAGAAAGGTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTCAGATATTTAGAT  
GTTTGTTACATTTTAAAAATTGCTCTTAATTTTAACTCTCAATACAATATATTTTGACC  
TTACCATTATTCCAGAGATTCAGTATTAACAAAAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTGCAT  
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQORMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC  
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCKGSKCKSKGYQGDLCSKPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGACAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG  
CCCCAGCCACACCTTACACAGGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCATTTCGCTACCGCCTGGGCACCA  
TCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG  
GTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTTCATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCGAAGCTGCTGTCTTGTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTTGCCTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATAACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG  
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG  
CGGACACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG  
GGGCGGTGACCCACGCCTCGCCCGACAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG  
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATAACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC  
TAATTTTTTGATTTTTTTGTAAAGAGGGGGGTCTCACTGTGTGCCCAGGCTGGTTTCGAAC  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA  
TAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC  
ALPYLGAIICYCDLFCNRTVSDCCPDFWDFCLGVPPPPFPPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRRHDQSHQPGQLWLAGWEPQRLLGHDGP

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## FIGURE 7

$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

## **FIGURE 8**

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCTTGGTTCTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA



### FIGURE 9

MTHTTTTWARRTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVYCTPVPHDPFPMALSRTPTRQISSSDT  
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFAHPHYDLSQVWSVVSPAPSRGQALRRAO

**Signal peptide:**

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

## **FIGURE 10**

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG  
CGTGTTACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTCATGGCCTTACAGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCCTTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGGACCAAGCGCACAC  
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCCGCCTCCC  
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG  
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT  
GAGTGTCACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC  
CGCTGAAAGGTCAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTTGTGTTGTTTGTGTTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCACCCCCAACTCCCAGCCC  
CGGAATAAAACCATTTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLE  
NNYTAFQONARHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGCTGTTTATTTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT  
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCTCT  
GAAGTCTTGGCTTATCATTTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTTCTGTCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAGAGTTCTCCATTGTCAGGAAAAC  
AATATTACAGACCATTTACCGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCAATTGTACGTAATTCGCTGTCC  
CACCCTCCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT  
AAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCACCACGACCCCCGGCCTG  
CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTC  
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA  
CAAACCTCATATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC  
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC  
CCAGAAGTGGAATAACAACCGGGGCGGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTTTGCTTTTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFP AELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLD DNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNMLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFN YRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC  
TCGCTTCCAGGCGCCGCGGCTGCAGCCTTGCCCCCTCTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACAGTGGGAGGTCCATCT  
CTAGGGGACAGACAGCTCGGACCCACCCGACAGCGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA  
TCTTGCAATTCTTGACATTGGTCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTCAATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCCCTGGAGCATAAAGTGTGCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCCTCAGAAAACCACGGATGTGAAC  
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAAA  
CGTGACAAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGAGCCACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCGTCTGCCAGTGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCCCTGTGAGTGTCTGAGGGACAGTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAACATTCGTGTGTAAAGCAGTGAAGATTCGTTTGTGT  
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGATTCGGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAACACATTTGTGTTA  
ATAATGGGAATTCTACATCTGCAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAAGTCTG  
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTACCCAAG  
GAGAAGGGGCCAGGCCCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTTACCCGACGGACGGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACATAAGAGATTGCCTCTGAGCCCAACAACAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG  
ATGAGATAAGTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAAC TGCCAAAAACGGTCCAACAGCCAAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAAATGTGAAAACTTATAATGT  
TCCAGAACCTTGCAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAATTCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGACAGAGCCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAAATCAGTACTGA  
GAAACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAATCCT  
TCAGAATTC TAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAATTCACCACTTCAG

1000 900 800 700 600 500 400 300 200 100 0

## **FIGURE 15**

MEKMLAGCFLLIILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALNKPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSALGDHGCE  
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVCCKSTHHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS  
PAGEPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMALLENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT  
TTCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT  
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATATGATGAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA



## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGANVTLSQCSPRSKPAVQYQ  
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL  
SSVTSARALRPPHGP RP GAL TPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

**FIGURE 18**

[illegible]

## **FIGURE 19**

MKRLPLLVVVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTETVVKTVNNFVQRDTFVVWDKLSVNHRRTHLTCLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGL  
LHYFFLAFAWMCIIEGILYLVVGVYINKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT  
TKVCWLSTENNFIIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

### FIGURE 20

$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCACCCCGGCTGGGA  
CAAGAAGCCGCCCGCTGCTGCGGGGCCGGGGAGGGGGCTGGGGCTGGGGCCGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGTTCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGAAGTGCAGCGCGGGG  
CAGAGCGCGCAGTTTGCTGGAGATCAAGGCGAGTCTGCTGCGGACCGTGGCCATCAAGGG  
CGTGACAGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTCAACGGACTGGAGGCGGTGAGGAGTCCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCTTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTAAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTTCTGTATGATGCTGTCTGCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC  
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAAATGGAGTTTGTTTGT

## **FIGURE 22**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLLEIKAVLRRTVAIKGVH SVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCTGGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAACTGGAAGT  
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG  
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCATCTCAAAAAATAAAATAAATAAATA  
AATAAATACTGGTTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDL NISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFOKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230



## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTTGGACAATG  
CAATTGTGGCACTGGCACCTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA  
TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTTAAGGGCCCATTTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA  
ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAAGCTCTATATTAATCACAAC  
TGCTTTCTACAATTTTACCTGGAGCCTTTATTTGGCCTACATAATCTTCTTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGTATGCTCTTCCAAATCTAGAGAT  
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAAGCCTCTTATCA  
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT  
GGACTGGAAAACCTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTGGATCTAAATAAAAATCCTATTATAGAA  
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC  
TACTAACAAACCCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTTCATCCGTTG  
GATGAACATGAACAAAACCAACATTTCGATTTCATGGAGCCAGATTCACTGTTTTGCGTGGACC  
CACCTGAATTTCAAGGTCAGAATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAAATGGCGTAACCTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG  
GCTCTTTGAATATTAAAAATAAGAGATATTTCAGGCCAATTCAGTTTTTGGTGTCTTGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAAATTTGTATTGATATTCACCACCATCTATCAGAAAAACAGAAAAAAA  
TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT  
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQLQTNNAKIEYSTDFVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNNLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDFYVHSEGLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAHV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKV KATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG  
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTTCAAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA  
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVNLNSKNGIEFIDEHAFKGVAETLQTLDSLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
NAANDADLCNLPKKTDDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT  
GGGCTCAGTGCTGTCAGGCTCGGCCACGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGGCG  
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT  
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCTCACC CGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT  
CATCGTCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA  
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA  
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCCGGCTCCTGTGGGTGTTCCGG  
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT  
GTGTGCCGGGCCGATGGCGACCCGCCGCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC  
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA  
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG  
TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC  
CTGGGCGTCGTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC  
AAAGCACAAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG  
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGGAGGGACCCCCG  
GGCGGCCGGGAGGGGAAGGGGCCTGGTCCGACCTGCTCACTCTCCAGTCTTCCCACCTC  
CTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG  
CCAGCCCTCACACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA  
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA  
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTTGGGTTTCAATAATTATGGATTTT  
TATGAAAACCTTGAAATAATAAAAAGAGAAAAAACTAAAAA

## **FIGURE 30**

MQVSKRMLAGGVSRMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLSLEQLTLEKCNLTSLIPTALSHLHGLIVLRLRHLNINAI RDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSI THCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGNLETILDSNPLA  
CDCRLLWVFRRRWRLNFNRRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAIWLSPRKHLVSAKSNGR LTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGND SMPAHLHVSYS PDWPHQPNKTF AFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCCGGGGATTCAGGCTCGCCAGCGCCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC  
TGTTTCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTTATTGTCTTCCTGCTG  
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTTAGAGGCGCCTGCCCACTTCCTGC  
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTTACAGAGCAA  
CCGAGGGCCGCCCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTTGTACTCGGTTTGGAAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTTCCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAACA

## **FIGURE 32**

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETTVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTCTG  
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT  
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA  
TCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTTCACTGCCCGACTTCCCAGTTTTACCATTTATTTCTGCATGGCAATTC  
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG  
CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTTAAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG  
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA  
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCCGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA  
GCTTTTCCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA  
ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA  
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT  
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT  
GTTTGTACCTCCGCCTTCACCGTGGTGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT  
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG  
ATACATCCTTCCCCACCGCAGGCACCCCGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG  
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAAACCGAAAGGGCCT  
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAATAAGTAACCTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPEYEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANS LPCPGGCSCDHIPGSG LKMNCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSFTVVGMLVFILNRNRKSRDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGCGCCTAAGGGAAACTGTTGGC  
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG  
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGCGG  
CGGCGAACACCCCCTGCGGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG  
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT  
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG  
GCCGCCTCTAACTTGAGCTATCGCGCGCCCTTCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG  
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACT  
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCCTCGATGGGGAT  
CACAGAGCAGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGTTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCCCGCCGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCTTGTGGCGGAGTCCCCCTCTTGGCTCTAGTGATGCATAGGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTTTCACTTTTGTATGAAACGGGGGAACCAAGAGGAACTTAC  
TTGTGTAAC TGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCCTTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA  
TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA  
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTAT  
ATTGGTTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS  
TVRAGAE LR AVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC  
CCCCGGCTACCTGGGCGCGCCCGCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAAC  
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTCTTATTCAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTTATTGGTCACTACATATTCAGGCCAAAA  
AAACTGCCTACAACACAGAACAGCCTGTCAACCACCACATTCCCTGTAACCACGGGTTTTAAA  
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAAACCATCACTCGCGATGGGAGTTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
TTAAAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT  
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT  
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTTATTTATACATCTCTGTAAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
GTTATTTGTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA  
AATCAATGCTTAATAAAATATTTTAAAGGAAAAAAAAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSTADGFIGHYIFRPKKLP TTTEQPVTTTTFPVT TGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCGCGGGCTGGGGCGGTTCGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG  
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTTCACAAGCAGCAGGAGGCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCCCTGTGCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG  
CTGGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT  
TCTGTGTTACCCACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA  
AAGGTCTTGGAAAGTTAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG  
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGP EESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG  
IIICALATLAAKGD LVFTAIFIGAVAAMTGYWLSERSDRVLEGF I KGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



[illegible]

AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT  
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTCTCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT  
CTTGGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTTCCTGGTGTGAGCCTGGTCCGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTTGTTTAAA  
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGAGGAATCTGCACTCAACTGCCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW  
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYS RGHFDR TKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAG  
GCTCGTGCCCACCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA  
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCACTGGGGTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC  
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCSDGSDEEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTTATTATGTGCGGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT  
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCTCCTGA  
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTC AAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG  
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT  
GTTGTTCCCTAAGAACTTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCTTTCTTCTTGGTTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSVLLLVLLLVLARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFRLN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCCGCGAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA  
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGAATGATGGCAGCATAT  
CACAATTTAGGAACCTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCTATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA  
CCGGTGCAACATGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTTCTTGCTCTATACAG  
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRLGGQPVCRRGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD FWIGLR RREEKQSNSTACQDL  
YAWTDGSISQFRN WYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLV  
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPS ESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCCTTGGGAGAGAGACTGAGGAAGAAGTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT  
CCCACTGATGAAGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

### **Signal sequence:**

amino acids 1-23

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

### **Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

### **Tyrosine kinase phosphorylation site.**

amino acids 280-288

### **N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

### **Amidation site.**

amino acids 216-220

### **Leucine zipper pattern.**

amino acids 10-32

### **Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCA  
GTCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACCTACATCA  
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVQCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

$\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} \nabla u \cdot \nabla v dx$

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTTCGGCTGCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
T TACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT  
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



1. *Principles of Mathematics* by David Hilbert. This work is a foundational text in the philosophy of mathematics, discussing the foundations of arithmetic and the role of axioms.

[illegible]

## **FIGURE 58**

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAIVIGYKMQA

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGGCTC  
AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCTGTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT  
GTTTCCATGCCACCTAAGGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC  
TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA  
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT  
AGCACGGGATTTATACAGTGCCTAATTAGTTTTTCCAGATATTTCTGAATATAAAAAATA  
ATGACTTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT  
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTGTCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCGAGA  
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA  
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT  
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC  
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA  
AATTTTAGGGTCTTGAATAGGAAGTTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGACAGTTG  
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAAGTTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA  
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA  
AAAATATTATATATAAAAGTAAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSL  
VGPFPG LNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F  
FQIFPEYKNND FYVTGESYAGKYVPAIAHLIHS LN P V R E V K I N L N G I A I G D G Y S D P E S I I G G  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIIYNGQLDIIVAAALTE R S L M G M D W K G S Q E Y K K A E K K V W K I F K S D S E V A G Y I R Q  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGKWD PYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT  
TTTTCCCTTTCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG  
TGAAC TTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCCTGGGTC  
AGGCCAGCCTCTTTGCTCCTCCCGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC  
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT  
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTGACCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCCTGTCCA  
GCCGGAAGCTGCCCCGAGACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTCCCTGCCCTTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC  
AGGCCTTCAATATCACCAAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG  
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTACCTCCTCAGCAAAGAGTCCCTCTTGGAAAGGTAGCTATTGGTGGAGATTAACTATAG  
GCAACTTTATTTTCTTGGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTTAATTTTGTG  
ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAAACCTTTAAGAAAAAAGTTTAAAGAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLP RDP ESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFL  
TVQPETPEGVAIN SAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSA LCAFP IRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLLKVRVYEFRC SNAIHLLSKE SLL EGSYWWRFNYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGC GGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA  
CGTGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCTGGTCGTCTTGGGCTTCCTGGTGTCC  
GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT  
GGAGGGACCGCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGCAGAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTACCGAAGCAGTGGACCTTTATTTTGACCACC  
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC  
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGTATGGAGT  
ACTGGACGGGGTGGTTTGACTCGTGGGAGGCCCTACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG  
GAGCCATGCACTTCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
TGTTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGGAATCTCTATCTGAATGATTCAACCTGAAAACCTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTTTCAAGGTTTCGGCCTGGACAAATGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA  
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAAAGACGCTTTACCTCCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGTTCATCGTTTTTGGAGAGACGATGGCGGGCCCTGCATTACAGTTCACGGAAACCCCCC  
ACCTGGGCAGGAACCAGTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC  
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG  
ACTGGGGGCTACAGTCTGCCCCGTCTCAGCTCAAAACCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC  
TGGCTTTGTGATGATGGCTTTTCTACAGCCCTGCTCTTGTGCCGAGGCTGTGCGGCTGTCTCTAGGGTGGGAGC  
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCCGACGTACAGCCC  
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTCTTGGAGGCTTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAAATCCTGGGTGTGTACCACTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCTTTCACAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCCTT  
TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC  
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA  
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG  
ACAGAAGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCCCAAGCAGGGGCAGAGCAGCCCTCCTTC  
GAAGTGTGTCCAAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCAAA

1000 900 800 700 600 500 400 300 200 100 0

## **FIGURE 64**

MTTWSLRRRPARTLGLLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLT TYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPMRLRTTYKGFTEAVDLYFDHLMSRVVPLQ  
YKRGGP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFD SWGGPHNILDSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE  
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSEFFQRFGLDKWXS L PETPTLP AFFLGSL SIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLP GPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTTCGTTCTAGTGGATAGGGGTTCATGACCGGTTTCTCCTAGACGGGGCCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC  
CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAGGTCTTGCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTTCAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTTTGGGCCAGCTGACAACATGACCAAATCTTTACCTTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTCTTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCTAGACTTGCTTTGCCCCCGTGGGCCCAT  
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC  
GAACCTATATGACCCATAACATTTTGGAGCCAAACACCATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCCATATGTGATGGTGGATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAG  
AGACAAACTATTTTGGACGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTTCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCGGTAAGTGGACAAAGCAGGGGCC  
ACAACAGACCCTCTACGTGCCAAGATTCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG  
TGCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCCTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLA GLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVD FGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM MYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTL YVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT  
CTTTGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT  
CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG  
AAAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTTCTCCACGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTACATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT  
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT  
GACTTGTTTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA  
AAAACCTTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG  
CTTGGAACCGCCTGCCAGCCCAGCTGGGCCAGTGTCGGATGCTCAAGAAAAGCGGGCTTGTTG  
TGGAAGATCACCTTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTTGCAAATGGGATTTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIPPLKEYSFEKVREESSFS DIPVKNDFAFL  
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHLFMLS G  
VPDAVFDLTDL DVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENKMGIGLESRLRLRHLKILHVKS NLTKVPSN  
ITDVAPHLTKLVIHNDG TKLLVLNSLKKMMNVAEELQNC ELERIPHAIFSLSNLQELDLKS  
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ  
KLRC LDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLS QLTQLELKGNC LDRLPAQLGQCRMLKKSGLVVEDH LFD TLPLEVKEALNQDINIP  
FANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCTTTTCATTGACAAACTGACTTTTTTTTATTTCT  
TTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTACACACATAAGGAT  
CTGTGTTTGGGGTTTCTTCTTCTCCCTGACATTGGCATTGCTTAGTGTTGTGTGGGGAGGGAGACCACGTGG  
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAATAACAAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCTGCTGCTGAGTGCTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCATCAGTTTTCATGGAAAATAACTCAGTGCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTGCGTCCCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA  
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAAGTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTGTAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAACTGT  
GGCGGTTACCTGGATACCTTGGGAAGGATCCTTCACAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT  
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCCCTAGAAATAGAC  
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTGACTGTGCTGTTGTCTACAGATTATGCCAATTCT  
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAACTTGACAGACCAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA  
TTTGAAAAGACTATACTTGAATCACCATAATTATGTGGATTGTAACCAAACCTTTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAATGCCTTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTGTATGTGAT  
AGCAGTGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCAGAAGCAAACGAGACATTTCTTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTTCGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT  
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTCTCTTCATGGTTCTAGCTCTG  
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGCCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

## **FIGURE 70**

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIIVKCEMGNST  
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFNQRADYKYQKLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGC  
TGCTGCCGCGCCGCGCCGTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC  
CTGGACGCCCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG  
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA  
AGATAACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT  
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGGCCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGACTGTACTATTCCCTTTTTGA  
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGGAAACTGCATGACAATAGACAAACTGTCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTTGAG  
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCCGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT  
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAACTACTGGGCCATGGACAGCCACTTAACTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATGC  
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACCTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCCACTA  
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC  
TCTTCACATTGATTTGTTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT  
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAAATACTGTAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA  
GTTTTTCTTTCTTCAATTATAAATAACATAAGTGTACTGTAACCTTTACAAACGTTTTAATT  
TTTAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295



## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGA TAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC  
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA  
TGGATTTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGAT  
ACTTGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCCCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC  
TGAACCATTGTTGAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC  
TATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTTCTTTCATGCTCC  
TTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT  
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCC  
TTTCTAGCCTGGCTATGTCTTAATAATATCCCCTGGGAGAAAGGAGTTTTTGCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG  
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC  
CCTTTCCTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA  
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA  
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTTGCTGAGACTAATCTT  
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG  
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA  
GCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA  
AGCATTTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLLTISIWTTRLLVQGSRLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTTCCGCTTGGATATTTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA  
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG  
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGTTCCTGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATC  
AGCTATTGAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCCTTCTTAG  
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC  
TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT  
TCCTTTTG

## **FIGURE 76**

MAVLAPLIAALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

Threat	Adaptation	Impact	Adaptation	Impact
Threat	Adaptation	Impact	Adaptation	Impact

[illegible]

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRRHLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPPVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as  $\epsilon \rightarrow 0$ . In the second part, we study the asymptotic behavior of the solutions of the system (1) as  $\epsilon \rightarrow 0$ . In the third part, we study the asymptotic behavior of the solutions of the system (1) as  $\epsilon \rightarrow 0$ .

[illegible]

## **FIGURE 80**

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL



## FIGURE 81

GGGGCCTTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGCGGGCGCGGGTGCAGAGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTCTGCTCCCAG  
CCTGTCTGTCTGTCGTTTGGCGCCCCCGCCTCCCGCGGTGCGGGGTGACACCCGATCCTG  
GGCTTCGCTCGATTGCGCGCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCAGGGGCTCT  
GAGGAGGTGACGCGCGGGGCTCCCGCACCTTGGCCTTGCCCGCATTCTCCCTCTCTCCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCGCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATG  
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT  
GGTCTGCTTCTTTCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAATGG  
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
GAAGGACCACATGTGGGCCTTGTTCAGGCCAGTGAACATCCCAAATAGAAATTTTACTTGAA  
AACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCTC  
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT  
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA  
CTTCTAGTAATTGTACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTTACAGGATT  
AGAACCAATTGTTTCTGATGTCATCAGAGGCATTTGTAGAGATTCTTAGAATCCCAGCAAT  
AATGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT  
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAATATTAAGTATGTCAAC  
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
ACTTTGTTAAAAACACTGCTGAGGCTTATAATCATGGCTCTTAGAACTCAGGAAAGAGGA  
GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCACAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF SVY  
GNIVYASVSSICGAAVHRGVI SN SGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLF AIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVT FVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKT FEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAF FTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

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## FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCCC  
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCCCGGCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA  
GGTTGAGGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC  
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT  
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA  
TCTTCTTCCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTCAGC  
TCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG  
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCTTGCTTTGCAAACATCAA  
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCACTTCTTCCATGGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTTCATCC  
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC  
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA  
TAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCCC  
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCCCGGCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA  
GGTTGAGGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC  
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT  
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA  
TCTTCTTCCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTCAGC  
TCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG  
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCTTGCTTTGCAAACATCAA  
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCACTTCTTCCATGGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTTCATCC  
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC  
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA  
TAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRS AVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRM LCTRDSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

## FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAACACACATGTGCATGTACACACACACATACA  
CACACATACACCTTCCTCTCCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTGAGTCAAAAAACATGGGAGGGG  
CCAGGCACGGTGACTCACCTGTAATCCCAGCATTTCGGGAGACCGAGGTGAGCAGATCACTTGAGGTGAGGAG  
TTCGAGACCAGCCTGGCCAAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT  
CAGCTGAGTGCACCGCTGCCTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA  
GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGCCCTGATGGGGCCTG  
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCCG  
GTGTAGAACTGACTGCCCTGGGAGGGTGGTTCCTTGGGCCCTGGCAGGGTGTGCTGACCCTTACCCTGCAAAACACA  
AAGAGCAGGATCCAGACTCTCCTTGTGAATGGTCCCCCTGCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC  
ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCTGGCATGTTCCTTGGCCCCCTCA  
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTACCGCGAGGCTACCCTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGGCCTCCCCGAGGCACACAGACCTGCTCCTGCAGAGCAACAGCATTGT  
CCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA  
TGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCT  
GGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTATCTCAACCACAACCAGCTCTACCGCATCGC  
CCCCAGGGCCTTTTCTGGCCTCAGCAACTTGTCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAG  
CCGCTGGTTTGAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT  
GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC  
CCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGGCCCCGGGTGCCAGGCGGGCACT  
GGAACAGGTGCCCGGGCTCAAGTTCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGC  
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGGCCTGGT  
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAAACCACGGCTGTCTTTCATCCACCCCGCGCCTTCCA  
CCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCAGTGCCTTGCAACCAGCAGACGGTGGAGTC  
CCTGCCCCAACCTGCAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCTATCCGCTGGGCCAATGC  
CACGGGCACCCGTGTCCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGGCCCTCATCTCCCCACGAAGCTTCCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGATTGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCAGGAGGTACCGGGGTACCCCGAGGGGACCCT  
GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACAC  
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCG  
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTACCCCCACCAACACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCCTCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCTGCTTCCGGGGAACCCACAGCTA  
CAACATTACCCGCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCACACCCCA  
GTTGGCTTGTGTATGGGCCAGGACCAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTTGGGCTCAT  
TGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCTGGGCTAGCGGGCCACCTTGGCACAGGCCAACCCAGGAA  
GGGTGTGGGTGGGAGGCGGCCTCTCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCCCTTCTGTCCGGGTTGT  
GTCTGCTCCCCCTCGTCTGCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACACTGTTGCC  
ACCATTGTCTCAAAATCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTTACCAAA  
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCCTGGCAGCTGGGC  
CAAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCCTCCCCATCTT  
CTCTCTGCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCCTACCTGTGTCCCCGGGCTGCACCCCTTCTCTTC  
TCTTTCTCTGTACAGTCTCAGTTGCTTGTCTTGTGCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC  
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA  
CGCCTCATCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA  
ATGTGTACCTCCCCCAACCCGATTCACTCTTTCTCCTGTTTTGTAAAAAATAAAAAATAAATAACAATAAA  
AAAA

1000 900 800 700 600 500 400 300 200 100 0

## **FIGURE 86**

MRLLVAPLLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLILLQSNISVRVDQSELGYLANLTDLSQLNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILD MNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPFSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTAEAGLYT  
CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLOVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT  
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC  
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGAGCTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA  
GCGCTTCGCCGTCTTCCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC  
CAGCATTGCCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT  
GGCCTTCCTGCGGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCCGCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA  
CGGCTGCGGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCA  
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAGCTCATCGTCTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT  
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCT  
AGCCATCAGGCCAACCCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT  
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG  
CAACCGGCTGGAGTGCTGCCTGTGGAGCTGGGCGAGTGCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA  
GGACCTGTTTAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG  
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCCGAGGGGCGAGGCCCTAGCTTCTCCAG  
AACTCCCGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTGGGGCTGGCCCCCTTCTCCCTCTGAGACTCAGTCCCCCAGGGCAAGTGCTTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCTCCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCCACCTCCTTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTCAGCCAGATGGAAGGTGTTGAGGGAAAGGTGGGCTGCCTTTTCCCC  
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG  
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA  
AAGGCCAGGCCTGGAGCTTGCTCTTCAGTTTTGTGGCAGTTTGTAGTTTTTGTTTTTTTTTTTTAAATCAAA  
AAACAATTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAAGAAAAAAACCTAAAAAA  
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT  
TGAAGTGTGTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTTGTTCTTGGGAGGGAGGTTTTTTTGTGTTGTTTTTGGGTTTTTTTTTGGTGTCTTGTCTTCTCTCTCC  
ATGTGCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGATGAACGGTGCTCCATTGCGACCTCCCTCCTCGTGCCTGCCCTGCCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTTCCCACTCCTGCGGCATGGGTGTGT  
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTTCATGAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTCCCGTCCCTGGCGC  
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCCTTAGATCAATCAGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAA

## **FIGURE 88**

MRQTIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSIDPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLMFMSGIPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ  
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447



## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTTCA GTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTCCGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAATAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG  
GGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAAGTGGGAAGGCCCTGT  
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELWGKAEMIIIEQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQORDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKCLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTGTTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

1000 900 800 700 600 500 400 300 200 100 0

## **FIGURE 92**

MGARGALLLALLLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW  
DSHVCVSVLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNK  
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT  
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCCGATCCCAG  
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAAGTGCCATTCT  
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGGACTGCACCGT  
TTTCCCCCAACATCATCCCTGAGGCAACGTCTTGAGCCGCAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGGTAACCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTCACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCCAGTTTCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGT  
GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG  
CCCCATATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATAACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTTCTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGGCCATTCCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC  
TGGGGAACACCAACTTCCCAGCTTTGCTTGAAGACTCTACTCAACCCCTGACCCTTTCTATC  
AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCTTAGATTCTCAATAAGATGCTGTAAGTAGCATTTTTTTGAATGCCTCTCCCTCCGC  
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA  
TTTCACTTGATATTCATTCCCCAATTCAGTGCAAGGAGACCTCTACTGTCACCGTTTACTCT  
TTCTTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG  
GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTTCTCTG  
ACTACTCTTGTCTTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC  
TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA  
TGTAACAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQQCHSVITQDFLTCWL  
SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSSNNSQACAQFLEQYFHSDSLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDSDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

[illegible]

CAAGAGATATGAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD  
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## **FIGURE 97**

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCACTGTTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCCAC  
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT  
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT  
CTCCAAAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACCTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGGTAAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCCCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG  
GGAACCTCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG  
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTGAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCACTCAAAGGG  
TGAAGAGGTGAGCTGTCCTCCTGTCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC  
GGGCCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGTAAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC  
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSP TASDMLHMRWDEE  
LAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSF RATEASDSRKMGT PSSLATGIPAF LVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSV  
SGLNSGPGHVWGPLLGLLLLLPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## FIGURE 101

GTAAGTGAAGTCAGGCTTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCAATTCTCCAAGTTATGTTGGACGT  
ACTTCTGTTGTTCTCCCTCTGCTTGCTTTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTCAT  
CAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAGTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA  
TTTGGCCAAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACT  
GCCCCAAGTGAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG  
TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTTGGGGGCTGAGCAA  
CATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT  
GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC  
ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTT  
GGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAAATGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATT  
GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAAACAATT  
TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGTCTGTAGCCAGA  
TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTT  
CAATTTGAGTTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGCTTGGAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAATTTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCAC  
CATCCTTCCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTTC  
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGATGACGTGTTCTTTATCGT  
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAAATGC  
AACTCTGACTGTCTAGAAACACCATCATTTTTCGCGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC  
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTTGGTGGT  
AACCAGAGAGGCATTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAA  
ATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC  
CTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGC  
CGTGGTTTGTGTGTGGTGGGCACGTCACTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCAGGGAACGTT  
AGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGG  
ATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC  
CACAGATCTGTTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA  
TCCTTTTGAACATATCATACAGGTTGCAGTCTTGACCCAAGAACAGTTTAAATGGACCACATGAGCCCAGTTA  
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATC  
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTACAATGAAGGACCTGGAATGAAAAATCTGTG  
TCTAAACAAGTCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTTCGGTTGCCTCGAGTAATCTTTTCATGGG  
TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCC  
AAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGAC  
AGATTTTCAGGAAGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA  
AAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGCTTTATTTATACAGAT  
GAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTA  
TTTTTTAACTTTGTTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTT  
TTATAATGCCAGATTTCTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACATTTT  
TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPV SAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRISAIPPKMFKLPLQHLLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLMLQELHLSQNAINRISPDAWE  
FCQKLSELDLTFNHL SRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRILIQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNFASQ  
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENY AHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKT PMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSP LVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDG  
WATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADI PSYLSSQGT LAD  
RQDGYVSSES GSHHQFVTSSGAGFFLPQH DSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYP CSHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

### **Signal sequence:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 746-765

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGCATAAAATAAATAATCTTAAAGCAGCTGTCCCCCTCC  
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAAGAAAAAAGTATGTTCATTTTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTTTTCTTTCTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGGAGAGAAAACAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTAAAT  
TTTTATTCTTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACACCTGGATTTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGTCT  
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
CCAGTTTCAGCAAGGTGATTTGTGTTTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCATAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGC  
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA  
TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGATGATACAGTCCCAGAT  
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACTG  
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG  
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCCGGCCTCCACATC  
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT  
GCTCAGTGATGGTACGTTAAATTTACAAATGTAAC'TGTGCAAGATACAGGCATGTACACATGTATGGTGGAGTAA  
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTC  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCC  
AGTGGTTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTTCGACAGAGAAAACCTT  
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT  
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGACCA  
TCGGCAAAACCATCACGCCCCAACCAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAACAACAGTTAAACACAATAAATTCAATACACAGTTTCACTGCATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAAATCAAAAAA  
GACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA  
AAAAGAAAAGAAATTTATTTATTTAAAAATCTATTGTGATCTAAAGCAGACAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGI STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNRLRYLNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN  
TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTF TIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537



# FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGACGCGACCGC  
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCGGGTGGGAGCTTCGGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCGCGGGGTTGGGGCTGCTGCTGTGC  
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGGTTCGCGGGGAACCTCGGGCAGCCCTCTGGGGTAGCCGCC  
GAGCGCCCATGCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT  
CCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTTCAAGCTCCAACTGCATTTCCAGCCCTACAG  
CTCAAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA  
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAAACTGCCCAACTGCAA  
CATCTGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCAAGGCCTTGGTGTCTGAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT  
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG  
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCATTACTAAAAAAGCCTTCACTGTTTGGATGCATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTCTTTTCAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATGCAATTTAAATACA  
TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAAACAATTTTCAAGCTTTGT  
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTCTGTAGCCAGATGGCTTTGTGTGT  
GATGATTTTCCCAAACCCAGATCACGGTTTCAAGCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC  
ATCTGCTCAGTGCCAGCAGCAGTGAATCCCAATGACTTTTGTCTGGAAAAAAGACAATGAATACTGCATGAT  
GCTGAAATGGAAATTTGTCAGTACCTCCGGGGCCAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCCGCTG  
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCAATCACTTTGGTTCATCCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCAGCTTGGAGTGTGCTGCTGTGGGGCACCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC  
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAAGCAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTTGGTGTGTAACCGAGAGGCAC  
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGCGGAAATACACATGTGAG  
ATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGGCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTGT  
GTGGTGGGCACGTCACTCGTGTGGGTGGTCACTATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC  
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTGACATCTTCAGGTGCTGGATTTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT  
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAACA  
TATCATACAGGTTGCAGTCTTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG  
GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC  
TCTTTAGATTTTGTGCAAAATCCAGAGCCAGCGTGGTTCCTCAGTAATCTTTTATGCGGTACCTTTGGAA  
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAAGAGCCTTTTAT  
TTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGGGAAGATGGGAAAGAAAGGACAGATTTTTCAGGAA  
GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAGAGAGAGAAT  
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATAC  
AAAAAGTTATGAAAATTTTATCTGGGAATGATGCTCATATAAGAATACCTTTTAAACTATTTTAACTTTG  
TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA  
TTTCTTTTTATGGAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTAAATAGAAGTT  
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 105: A sequence of nucleotide bases (A, T, C, G) arranged in a single line. The sequence is 1000 bases long and contains several stop codons (TAA, TAG, TGA) which are underlined. The sequence is: AGCCGACGCTGCTCAAGCTGCAACTCTGTTGAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGACGCGACCGC GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCGGGTGGGAGCTTCGGGTAGA GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCGCGGGGTTGGGGCTGCTGCTGTGC GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGGTTCGCGGGGAACCTCGGGCAGCCCTCTGGGGTAGCCGCC GAGCGCCCATGCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT CCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTATCAAGGCAAGTTCC ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG TTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTTCAAGCTCCAACTGCATTTCCAGCCCTACAG CTCAAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAAACTGCCCAACTGCAA CATCTGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCAAGGCCTTGGTGTCTGAAGTCT CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG AACAAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC AATGAAATTTCTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC CAAGGAAATCGGATCCGTTCATTACTAAAAAAGCCTTCACTGTTTGGATGCATTGGAGCATCTAGACCTGAGT GACAACGCAATCATGTCTTTTCAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATGCAATTTAAATACA TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAAACAATTTTCAAGCTTTGT AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTCTGTAGCCAGATGGCTTTGTGTGT GATGATTTTCCCAAACCCAGATCACGGTTTCAAGCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC ATCTGCTCAGTGCCAGCAGCAGTGAATCCCAATGACTTTTGTCTGGAAAAAAGACAATGAATACTGCATGAT GCTGAAATGGAAATTTGTCAGTACCTCCGGGGCCAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCCGCTG CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCAATCACTTTGGTTCATCCTACTCTGTC AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC ATGGCAGCTTGGAGTGTGCTGCTGTGGGGCACCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAAGCAATGCAACTCTGACTGTC CTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTTACAGTGC ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTTGGTGTGTAACCGAGAGGCAC TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGCGGAAATACACATGTGAG ATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCT CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGGCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTGT GTGGTGGGCACGTCACTCGTGTGGGTGGTCACTATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCAGGGAACGTTAGCTGACAGGCAG GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTGACATCTTCAGGTGCTGGATTTTTCTTACCA CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAACA TATCATACAGGTTGCAGTCTTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC TCTTTAGATTTTGTGCAAAATCCAGAGCCAGCGTGGTTCCTCAGTAATCTTTTATGCGGTACCTTTGGAA GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAAGAGCCTTTTAT TTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGGGAAGATGGGAAAGAAAGGACAGATTTTTCAGGAA GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTTCAGTCTTATGACTTGGAC ACATAGACTGAATGAGACCAAGGAAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAGAGAGAGAAT CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATAC AAAAAGTTATGAAAATTTTATCTGGGAATGATGCTCATATAAGAATACCTTTTAAACTATTTTAACTTTG TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA TTTCTTTTTATGGAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTAAATAGAAGTT ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLOHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSOMK  
KLQQLHLNTSSLLCDCQLKWL PQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCDFF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQGG  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERRGNVRLSVIPTPTCDSPQMTAPSLDDDGWA  
TVGVVIIAVVCCVVGTSVLVWVVI IYHTRRRNEDCSITNTDETNPADIPSYLSSQGT LADRQ  
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKG NVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 808-828

### **N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### **Glycosaminoglycan attachment site.**

amino acids 886-890

### **Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### **Tyrosine kinase phosphorylation site.**

amino acids 667-675

### **N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### **Leucine zipper pattern.**

amino acids 58-80, 65-87

# FIGURE 107

CAAAACCTTGCGTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCCGAGCCCCGCGGAGCGCAGCTGAGAC  
 TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
 CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCCGTTGGTGGTCCCGTCCCCTATCCCTCCTTTATATA  
 GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAAGGAGGCGCGCTGATCTGCAG  
 GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
 TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGGTGCTGC  
 TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA  
 GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACAATTTGCGGAGGAGGAGCCGTGCTGGTACTGAGCCCTGAGG  
 AGCCCGGGCCTGGCCAGCCGCGGTTCAGCTGCCCCCGAGACTGTGCTGTTCCAGGAGGGCGTCTGTGGACTGTG  
 GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACCAACCAGC  
 TGGAAAAGATCTACCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA  
 CTTCCCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTTGGCCAATAACAAGC  
 TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT  
 ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC  
 TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCCTCATCCTGTCCAGCAACTTCCCTGCGCCACGTGC  
 CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT  
 TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACCTGACTGACTGACGAGGGCCTGGACAACGAGA  
 CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC  
 CGCGCAGCCTGGTGTGCTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
 GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC  
 TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCTGCCAGTGGCCTGCCCTGCCCGCGTGC  
 GCACCCCTCATGATCCTGCACAACAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTCTGGAGG  
 AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGCGACGCTTCCGCAAGCTGCGCCTGCTGC  
 GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
 TCAAGCGCAATGAGCTGGCTGCCTTGGCAGCAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
 CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA  
 TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAACA  
 AGATTAGTGCGGTGCCCGCAATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGC  
 TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
 TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
 AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTTCTGC  
 AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
 TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGC  
 ACACACATCACACCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCAAACACCCACAGTCTCTGTACAC  
 CCCCCTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCACCCCA  
 TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA  
 CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
 GTCCATCTGTCCGTCCGTTCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCCTCT  
 GGAACTCACAAAAGCTGGCTTTTATTCCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
 TGGCCACCCCTGCTCCTCCAGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
 CAGGCACCTTTTCCAATGGGCAAGCCAGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 GTTCTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCCTTATTTTATTTTCTTTCTAAGGAAAAAATGATAAAAAT  
 CTCAAAGCTGATTTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

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## **FIGURE 108**

MEGEEAEQPAWFHQPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPREENEFAEEEPVLVLSPPEPGPGPAAVSCPRDCACSQEGVVDCCGIDLREFPGDLP  
EHTNHLSQLNNQLEKIYPEELSRHRLETNLQNNRLTSRGLPEKAFFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVLDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF  
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

[illegible]

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCTCCGGGAGCGGCAG  
CAGTAGCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCACCACCC  
CAACCTGTTCTCTCGCGCGCACTGCGCTGCGCCCCAGGACCCGCTGCCCAACATGGATTTCCTCTGGCGCTGGT  
GCTGGTATCTCTGCTCTACCTGCAAGGCGGCGCGAGTGTGCAGCGGAGGTTGCCCCAGGCAAAATAGTGTATCGAT  
TGGCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTACAGCC  
TGTGTGCGCAACACCATGATGCAAAATGTTGTAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA  
CGGCAGCTACAAGTGTACTGTCTCAACGGATATATGCTCATGCCGATGGTTCTCTGCTCAAGTGCCTTGACCTG  
CTCCATGGCAAACTGTGAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGCCCT  
GCACCTGGCTCTCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCTGCCCCTAGATT  
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTATGAAGGCTTCGATCTCATGTATATTGGAGG  
CAAAATATCAATGTATGACATAGACGAATGCTCACTTGGTTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA  
CGTACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAA  
AGTTATGATTGAACCTTCAGGTCCAATTTCATGTACCAAAGGAAATGGTACCAATTTTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTTACCAA  
CAGGCTTACTTCTAAGCCCAACAAGACCTTACCAAAAGCCAAACCAATCTTCTACTCCACCACCACCCACCC  
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAAACCCGAGAAAGGCCAACCCGGACTGCAACTATAGC  
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGG  
AGATGTGTTTCAGTGTCTGTTGTTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCCTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTTCGGCAGCCAAAGCCCCAGG  
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCACTCAGGGGACCTGTGCCCTGTCTTTCAGGCCA  
CAGAGTACAGGGGCTGCACTCTGGCACCTCCAGGTGTTGTGAGAAAACAGGTCGCCACGGAGCAGCCCTGTG  
GGGAAGAAATGGTGGCACTGGCTGGAGCAGCAACAGATCACTTTCGAGAGGGCTGACATCAAGAGCGAATCACA  
AAGATGATTAAGGGGTTGGAAAAAAGATCTATGATGGAAAAATTAAAGGAACTGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGAGGGGCAAAACATTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG  
TCTCCATATGCACTAAGAATAGAAACAAGAGGAACTGGCTTAGACTAGAGTATAAGCGGAGCATTTCTTGGCAGG  
GGCCATTGTTAGAATACTTCATAAAAAAAGAGTGTGAAAAATCTCAGTATCTCTCTCTTTCTAAAAAAATTAGA  
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCAAGGAAAGATACCAAAATTATAGAATTTCCCAA  
AGATGTTTTGATCCTACTAGTAGTAGTGCAGTGAAAAATCTTGAAGATAAATAATTTGGACAAGGCTTAATTTAGG  
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCCACCAATGCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC  
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTTCTTCATGGTAAAGGTATAAGCC  
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTAAAGAGATCTTCAAGGAACACAGTTCAGAGAG  
ATTTTCATCGGGTGCACTCTCTGCTGCTGTGTGACAGTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC  
ACACCGGCAGACCTTTCTTTCACCTCATCAGTATGATTGAGTTTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTTAACCTGGTAAAGGCAGGGCTGG  
AGGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTAAATGGTTCATT  
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAAATGAAAAATTTTACCTTTTCATGCCCCA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGGTTTATTATTATTAAATGGTTT  
CTAAAATAAAAAATGTTAGTGGTTTTTCCAAATGGCCTAATAAAAAACAAATTTTGTAAATAAAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGN GTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTLRTPLPPTTPTTGLTTIAPAAS TTPPGGITVDN  
RVQTD PQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG  
KAARLVLP LGRMLHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACTTTCCCTTTGCAACAGGTGCTTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC  
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGAGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCGAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT  
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT  
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACTTTCATGG  
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA  
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAAACTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG  
TTAAGAATGCTAAATTTATGTTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA  
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACCTATGCCTTCTCTTTTTTTTCAATCACC  
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA  
TTTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGCTGTT  
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC  
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCGTTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGTGTTTGAAGTG  
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT  
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTG  
TTTCACTGTGTGAAAAAAGAAGATATTTCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG  
AAATGTGTATTTCACTGACAATTTCTGGTCTTTTTTAGAGGTATATTCCAAAATTTCTCTGT  
ATTTTTAGGTTATGCAACTAATAAAAACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAAGTTCATGGTATTCTCTTGATTC  
CAACAAAGTTTGATTTTCTCTGTATTTTTCTTACTTACTATGGGTACATTTTTTTATTTTT  
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTTGT  
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT  
TTGGCCACTTTTTTTCAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTGTTTTTTT  
TTTCTTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGA  
TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG  
CATCTTCTTGATATATGTCTTAAATGTATTTTTTGTCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTTTATATTTTTTAAAGACAA  
ACTTCATATTATCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGATTTACAGGTAATA  
GTCAGTAGGATGGAACATTTTAGTGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT  
CACCTTAAAGAAGGGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGTCCCCTTCTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG  
TATCGTAATATAACAAGTTTTCTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT  
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE  
EEAESKEGTNKDFPQNPAIRQPSLGPSTLTDKS

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 182-201

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### **Tyrosine kinase phosphorylation site.**

amino acids 107-115

### **N-myristoylation site.**

amino acids 20-26, 192-198

### **Amidation site.**

amino acids 25-29

114

## FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTAACTAATTCAACAAACGGGACCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG  
AAGGTCTTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG  
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA  
GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCGTGGG  
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTACTGTCGCCAGCTA  
CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACCTTCGACTTCTCTAGGCGACCTTTTGACAGCGG  
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTAGTAGAGCTG  
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCCC  
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCTTTTCTGTCTTCCCCTTCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTTCTATCAGGCT  
GATTTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCCATTGAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT  
GGCATTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKMRLQDQTYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEVGLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTACTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTGGGGATGCTGGTCTGGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCC  
CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC  
CCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTCTGGATCCAGGGGGAGGGAGAAG  
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGTGTTGGCTGTCTTGACCTCCCGAGCTACACTGTCCA  
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCAGTGGGCAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCCGCTGGCTCATGTGAGAGCCCTGC  
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGCAGGATGACACATATGTGCAGGCCC  
CCCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTCAATTG  
GCGCAGGCGAGCAGGCCCGGTACTGTGTCATGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGC  
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTAGTGGCGCTCCTGACGAGTGGCTTGACGCTCATTG  
ACTCTCTGGGCGTGGCTGTGTCTCACAGCACAGGGGGCAGCAGTATCGCTCATTTGAACTGGCCAAAAATAGGG  
ACCTTGAGAAGGAAGGGAGCTCGGCTTTCTGAGTGCCTTCGCCGTGCACCCTGTCTCCGAAGGTACCCTCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACTGCAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCCGTGGGGCTCCCTGCTCCTTTCA  
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG  
CTCCCAAGTGCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGGCGCTATCAGCCCCGCTTCCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAC  
GGGGCATGGAGTACACCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCA  
GGGTGAGCCTGCTGCGGCCACTGAGCCGGGTGGAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC  
AGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCTCGAGGCGTTTGCAGCCAATGTCC  
TGGAGCCACGAGAACATGCATTGCTCACCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCG  
CTGTGCGAGCAGAGGCCCCCTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCTGTGGACACTCTCT  
TCTTCCTTACCACCGTGTGGACAAGGCCTGGGCCCCGAAGTCTCAACCGCTGTGCGCATGAATGCCATCTCTGGCT  
GGCAGGCCTTCTTTCCAGTCCATTTCAGGAGTTCAATCCTGCCCTGTACCAACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGTGACCCCTCCCGGGGGGCTCCTATAGGGGGGAGATTTG  
ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGGCCGAGCCCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCGGTTCTCAGGGCTCC  
ACCTCTTTTGGGCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCTGCGAGACTGCAGCCACGGCTCAGTGAAG  
AACTCTACCACCGCTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGGCCCTAACCTCATTACCTTCTCTTGTCTGCCTCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAATGTTATTAA  
ACATGTCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPD SRARLD  
QSD EDFKPRIVPYRDPNKP YKKVLRTRYIQTELGS RERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSR SLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLT VLTPEGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCP LQGASRADVGDALETALEQLNRRYQPR LRFQKQRLNNGYR  
RFD PARGMEYTLDLLLEC VTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATR VQLVLP LL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKAAA AELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVS KKHVPDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAE GCFYNADYLAA  
RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQE QANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG  
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG  
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAAGTCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTTTCTTTTTCTTTCTAATTTGGTGCGACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATG  
TGTGGAAGAAGTGTTTTAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTTGCTGATTGGTT  
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAATAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250



[illegible][illegible]

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCCTGACTTCTTCTCTGCTGCTGCTTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCAAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGC  
AGACAAGTGACCCCAAGATCGAGTGGAAGAAAAATCAAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCTGTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCAGTACAGCTGGTATCGCAATGATGTACCCTGCCACGGATT  
CCAGAGCCAATCCAGATTTTCGCAATTCCTTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTTGGCGGAATTATTTGGGGGGGTTCTGGTTGTCTTGTCTGACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGATGATGCACTCGGACAGAGCTAGACACTCATTAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTCAACACTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAACAAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCCTGAGGAACCCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTAAAGGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCCCTTTCT  
CACACAAGTTTGTAGCCTTTTTCACAAGGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTAGCTTTGAAC  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCAGAAAATAGGGCCCCCAATGCTATTTTTTTTTTAAAGTTGTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAAGAAAATGGAT  
CCCACTGTTCTCTTTGCCACAGAGAAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAAGCAGTTTCTAATTTTGAATTTTAAATTTTTCATCCGCCGAGACACTGCTCCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA  
GAATGGCTCTCACTACTACCTTGCTTTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTTGCCGAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC  
CTCATTTATAAAAGCTTCAAAAAAACCCA

## FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVPVCRVPAKVPVKGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267